



#C

SEQUENCE LISTING

<110> Denney, Jr., Dan W.
<120> Vaccines for Treatment of Lymphoma and Leukemia
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<140> 09/925,192
<141> 2001-08-09
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att agc gat gat gaa cca ggt tat gac cta gat ttg ttt tgt ata cct 162
Ile Ser Asp Asp Glu Pro Gly Tyr Asp Leu Asp Leu Phe Cys Ile Pro
10                      15                      20                      25

aat cat tat gcc gag gat ttg gaa aaa gtg ttt att cct cat gga ctg 210
Asn His Tyr Ala Glu Asp Leu Glu Lys Val Phe Ile Pro His Gly Leu
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att atg gac agg act gaa aga ctt gct cga gat gtc atg aag gag atg 258
Ile Met Asp Arg Thr Glu Arg Leu Ala Arg Asp Val Met Lys Glu Met
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 35 40 45

Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala
 50 55 60

Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp
 65 70 75 80

Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr
 85 90 95

Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly
 100 105 110

Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys
 115 120 125

Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln
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Thr Leu Leu Ser Leu Val Lys Gln Tyr Ser Pro Lys Met Val Lys Val
 145 150 155 160

Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Val Gly Tyr Arg Pro
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Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala
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 <222> (13)..(573)

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 15 20 25

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 Asn Glu Phe Lys Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu
 30 35 40 45

ggt aaa cag aat ctg gtg att atg ggt agg aaa acc tgg ttc tcc att 195
 Gly Lys Gln Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile
 50 55 60

cct gag aag aat cga cct tta aag gac aga att aat ata gtt ctc agt	243
Pro Glu Lys Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser	
65 70 75	
aga gaa ctc aaa gaa cca cca cga gga gct cat ttt ctt gcc aaa agt	291
Arg Glu Leu Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser	
80 85 90	
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Leu Asp Asp Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys	
95 100 105	
gta gac atg gtt tgg ata gtc gga ggc agt tct gtt tac cag gaa gcc	387
Val Asp Met Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala	
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Met Asn Gln Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln	
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Glu Phe Glu Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr	
145 150 155	
aaa ctt ctc cca gaa tac cca ggc gtc ctc tct gag gtc cag gag gaa	531
Lys Leu Leu Pro Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu Glu	
160 165 170	
aaa ggc atc aag tat aag ttt gaa gtc tac gag aag aaa gac	573
Lys Gly Ile Lys Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp	
175 180 185	
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Lys Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu Gly Lys Gln	
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Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile Pro Glu Lys	
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Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser Arg Glu Leu	
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Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser Leu Asp Asp
85 90 95

Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys Val Asp Met
100 105 110

Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala Met Asn Gln
115 120 125

Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln Glu Phe Glu
130 135 140

Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr Lys Leu Leu
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Lys Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp
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 <222> (1)..(744)

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 Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
 20 25 30
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 Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
 35 40 45
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 Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60
 gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag 240
 Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
 65 70 75 80
 gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa 288
 Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
 85 90 95
 atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca 336
 Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
 100 105 110
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 Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
 115 120 125
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 130 135 140
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 Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
 145 150 155 160
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 Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
 165 170 175
 ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac 576
 Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
 180 185 190

tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca	624
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro	
195 200 205	
agc cct ctc cca aat aaa gga agt gga acc act tca ggt act acc cgt	672
Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg	
210 215 220	
ctt cta tct ggg cac acg tgt ttc acg ttg aca ggt ttg ctt ggg acg	720
Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr	
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cta gta acc atg ggc ttg ctg act tag	747
Leu Val Thr Met Gly Leu Leu Thr	
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20 25 30

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35 40 45

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
50 55 60

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
65 70 75 80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
85 90 95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
100 105 110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
115 120 125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
130 135 140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145 150 155 160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
165 170 175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
180 185 190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
195 200 205

Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg
210 215 220

Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr
225 230 235 240

Leu Val Thr Met Gly Leu Leu Thr
245

<210> 28
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 28
ccacttcctt tatttggtgc agattcag

28

<210> 29
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> CDS
<222> (1)..(783)

<400> 29
atg gtg tgt ctg aag ctc cct gga ggc tcc tgc atg aca gcg ctg aca
Met Val Cys Leu Lys Leu Pro Gly Gly Ser Cys Met Thr Ala Leu Thr
1 5 10 15

48

gtg aca ctg atg gtg ctg agc tcc cga ctg gct ttg gct ggg gac acc
Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr
20 25 30

96

cga cca cgt ttc ttg tgg cag ctt aag ttt gaa tgt cat ttc ttc aat	144
Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn	
35 40 45	
ggg acg gag cgg gtg cgg ttg ctg gaa aga tgc atc tat aac caa gag	192
Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu	
50 55 60	
gag tcc gtg cgc ttc gac agc gac gtg ggg gag tac cgg gcg gtt gag	240
Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu	
65 70 75 80	
gag ctg ggg cgg cct gat gcc gag tac tgg aac agc cag aag gac ctc	288
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu	
85 90 95	
ctg gag cag aag cgg ggc cag gtg gac aat tac tgc aga cac aac tac	336
Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr	
100 105 110	
ggg gtt ggt gag agc ttc aca gtg cag cgg cga gtt gag cct aag gtg	384
Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val	
115 120 125	
act gtg tat cct tca aag acc cag ccc ctg cag cac cac aac ctc ctg	432
Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu	
130 135 140	
gtc tgc tct gtg agt ggt ttc tat cca ggc agc att gaa gtc agg tgg	480
Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp	
145 150 155 160	
ttc cgg aac ggc cag gaa gag aag gct ggg gtg gtg tcc acg ggc ctg	528
Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu	
165 170 175	
atc cag aat gga gat tgg acc ttc cag acc ctg gtg atg ctg gaa ata	576
Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile	
180 185 190	
gtt cct cgg agt gga gag gtt tac acc tgc caa gtg gag cac cca agt	624
Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser	
195 200 205	
gtg acg agc cct ctc aca gtg gaa tgg aga gca cgg tct gaa tct gca	672
Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala	
210 215 220	
cca aat aaa gga agt gga acc act tca ggt act acc cgt ctt cta tct	720
Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser	
225 230 235 240	
ggg cac acg tgt ttc acg ttg aca ggt ttg ctt ggg acg cta gta acc	768
Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr	
245 250 255	
atg ggc ttg ctg act tag	786
Met Gly Leu Leu Thr	
260	

<210> 30
 <211> 261
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 30

Met Val Cys Leu Lys Leu Pro Gly Gly Ser Cys Met Thr Ala Leu Thr
 1 5 10 15

Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr
 20 25 30

Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn
 35 40 45

Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu
 50 55 60

Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu
 65 70 75 80

Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
 85 90 95

Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr
 100 105 110

Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val
 115 120 125

Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
 130 135 140

Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
 145 150 155 160

Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu
 165 170 175

Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile
 180 185 190

Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
 195 200 205

Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
 210 215 220

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
 225 230 235 240

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
 245 250 255

Met Gly Leu Leu Thr
 260

<210> 31
 <211> 189
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> CDS
 <222> (1)..(186)

<400> 31
 ttg gat cca cga tcg ttt cta ttg cgc aat cca aat gat aag tac gaa 48
 Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
 1 5 10 15
 cca ttt tgg gaa gat act aca gag aac gtg gtg tgt gcc ctg ggc ctg 96
 Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu
 20 25 30
 act gtg ggt ctg gtg ggc atc att att ggg acc atc ttc atc atc aag 144
 Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys
 35 40 45
 gga gtg cgc aaa agc aat gca gca gaa cgc agg ggg cct ctg taa 189
 Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu
 50 55 60

<210> 32
 <211> 62
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 32

Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
1 5 10 15

Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu
20 25 30

Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys
35 40 45

Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu
50 55 60

<210> 33

<211> 192

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1)..(189)

<400> 33

ttg gat cca cga tcg ttt cta ttg cgc aat cca aat gat aag tac gaa 48
Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
1 5 10 15

cca ttt tgg gaa gat cag agc aag atg ctg agt gga gtc ggg ggc ttc 96
Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe
20 25 30

gtg ctg ggc ctg ctc ttc ctt ggg gcc ggg ctg ttc atc tac ttc agg 144
Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg
35 40 45

aat cag aaa gga cac tct gga ctt cag cca aca gga ttc ctg agc tga 192
Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser
50 55 60

<210> 34

<211> 63

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 34

Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
1 5 10 15

Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe
20 25 30

Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg
35 40 45

Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser
50 55 60

<210> 35

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 35

cgatcgtgga tccaagtta gggtcgtatc tgtttcaaa

39

<210> 36

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 36

cgatcgagga tccaagatgg tggcagacag gacc

34

<210> 37

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 37

acgcgtccac catggccata agtggagtcc ct

32

<210> 38

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 38
 ggatccaact ctgtagtctc tgggagag 28

<210> 39
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 39
 acgcgtccac catggtgtgt ctgaagctcc tg 32

<210> 40
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 40
 ggatccaact tgctctgtgc agattcaga 29

<210> 41
 <211> 292
 <212> DNA
 <213> Homo sapiens

<400> 41
 gaattctttt ttgcgtgtgg cagttttaag ttattagttt ttaaaatcag tacttttttaa 60
 tggaaacaac ttgacaaaaa atttgtcaca gaattttgag acccattaaa aaagttaaat 120
 gagaaacctg tgtgttcctt tggtaaacac cgagacattt aggtgaaaga catctaattc 180
 tggttttacg aatctggaaa cttcttgaaa atgtaattct tgagttaaca cttctgggtg 240
 gagaataggg ttgttttccc cccacataat tggaagggga aggaatatcg at 292

<210> 42
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 42
 tcgatggcgc gccttaatta 20

<210> 43
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 43
 agcttaatta aggcgcgcca

20

<210> 44
 <211> 1147
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 44
 gcggccgcgt cgaccaaggg ccccgagcgtg ttccccctgg cccctgctc ccgcagcacc 60
 agcggcggca ccgccgccct gggctgcctg gtgaaggact acttccccga gcccgtagacc 120
 gtgagctgga acagcggcgc cctgaccagc ggcgtccaca ccttccccgc cgtgctgcag 180
 tccagcggcc tgtactccct gagcagcgtg gtgaccgtgc ccagcagcag cctgggcacc 240
 cagacctaca cctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagcgcgtg 300
 gagctgaaga cccccctggg cgacaccacc cacacctgcc cccgctgccc cgagcccaag 360
 agctgcgaca cccctcccc ctgccccgc tgccccgagc ccaagagctg cgacaccct 420
 cccccctgcc cccgctgccc cgagcccaag agctgcgaca cccctcccc ctgccccgc 480
 tgccccgccc ccgagctgct gggcggcccc agcgtgttcc tgttcccccc caagcccaag 540
 gacaccctga tgatctcccg ccccccgag gtgacctgcg tggtagtgga cgtgagccac 600
 gaggaccccc aggtgcagtt caagtgttac gtggacggcg tggaggtgca taacgcccaag 660
 accaagcccc gcgaggagca gtacaacagc accttccgcg tggtagcgt gctgaccgtg 720
 ctgcaccagg actggctgaa cggcaaggag tacaagtgca aggtgagcaa caaggccctg 780
 cccgccccca tcgagaagac catctccaag accaagggcc agccccgcga gcccagggtg 840
 tacaccctgc ccccgagccg cgaggagatg accaagaacc aggtgagcct gacctgcctg 900
 gtgaagggct tctaccccag cgacatcgcc gtggagtggg agagcagcgg ccagcccag 960
 aacaactaca acaccacccc ccccatgctg gacagcgacg gcagcttctt cctgtacagc 1020
 aagctgaccg tggacaagag ccgctggcag cagggaaca tcttctcctg cagcgtgatg 1080
 catgaggccc tgcacaaccg cttcaccag aagagcctga gcctgagccc cggcaagtga 1140
 tagatct 1147

<210> 45
 <211> 377
 <212> PRT
 <213> Homo sapiens

<400> 45

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
 100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
 115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
 130 135 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
 145 150 155 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
 195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 210 215 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375

<210> 46
<211> 999
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 46
gcggccgcgc gtcgaccaag ggccccagcg tgttccccct ggccccctgc agccgcagca 60
ccagcgagag caccgccgcc ctgggctgcc tgggtaagga ctacttcccc gagcccgtga 120
ccgtgagctg gaacagcggc gccctgacca gcggcgtgca caccttcccc gccgtgctgc 180
agagcagcgg cctgtactcc ctgagcagcg tggtagaccgt gccagcagc agcctgggca 240
ccaagaccta cacctgcaac gtggaccaca agcccagcaa caccaaggtg gacaagcgcg 300
tgagagagcaa gtacggcccc ccctgccccca gctgccccgc ccccgagttc ctgggcggcc 360
ccagcgtggt cctgttcccc cccaagccca aggacaccct gatgatcagc cgcacccccg 420

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aggtgacctg cgtggtggtg gacgtgagcc aggaggaccc cgaggtgcag ttcaactggt 480
acgtggacgg cgtggagggtg cataacgcca agaccaagcc ccgcgaggag cagttcaaca 540
gcacctaccg cgtggtgagc gtgctgaccg tgctgcacca ggactggctg aacggcaagg 600
agtacaagtg caaggtgtcc aacaagggcc tgcccagcag catcgagaag accatcagca 660
aggccaaggg ccagccccgc gagccccagg tgtacaccct gccccccagc caggaggaga 720
tgaccaagaa ccaggtgagc ctgacctgcc tggatgaagg cttctacccc agcgacatcg 780
ccgtggagtg ggagagcaac ggccagcccg agaacaacta caagaccacc cccccctgc 840
tggacagcga cggcagcttc ttcctgtaca gccgcctgac cgtggacaag agccgctggc 900
aggagggcaa cgtgttctcc tgctccgtga tgcattgagg cctgcacaac cactacaccc 960
agaagagcct gagcctgagc ctgggcaagt gatagatct 999

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<210> 47
<211> 327
<212> PRT
<213> Homo sapiens

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<400> 47

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```

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1          5          10          15

```

```

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
          20          25          30

```

```

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
          35          40          45

```

```

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50          55          60

```

```

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65          70          75          80

```

```

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
          85          90          95

```

```

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
          100          105          110

```

```

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
          115          120          125

```

```

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
          130          135          140

```


Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325

<210> 48

<211> 337

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 48
 gcggccgcac tgtggctgca ccattctgtct tcattcttccc gccattctgat gaggcagctta 60
 agtccggaac cgccagcgtg gtgtgcctgc tgaacaactt ctacccccgc gaggccaagg 120
 tgcagtggaa ggtggacaac gccctccaga gcggcaactc ccaggagagc gtgaccgagc 180
 aggacagcaa ggacagcacc tacagcctga gcagcaccct gaccctgagc aaggccgact 240
 acgagaagca caaggtgtac gcctgcgagg tgacccatca gggcctgagc agccccgtga 300
 ccaagagctt caaccggggc gaggctagtg gagatct 337

<210> 49
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 49

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1 5 10 15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 20 25 30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 35 40 45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 100 105

<210> 50
 <211> 346
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

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<400> 50
gcggccgcac cgtcctaggt cagcccaagg cggcgcccag cgtgaccctg ttccccccca      60
gcagcgagga gctgcaggcc aacaaggcca ccctggtgtg cctgatcagc gacttctacc      120
ccggggccgt gaccgtggcc tggaaggccg acagcagccc cgtgaaggcc ggcgtggaga      180
ccaccacccc cagcaagcag agcaacaaca agtacgccgc cagcagctac ctgagcctga      240
cccccgagca gtggaagagc caccgcagct acagctgcca ggtcaccac gagggcagca      300
ccgtggagaa gaccgtggcc cccaccgagt gcagctagtg agatct                        346

```

```

<210> 51
<211> 109
<212> PRT
<213> Homo sapiens

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```

<400> 51

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```

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro
1          5          10          15

```

```

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
20          25          30

```

```

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
35          40          45

```

```

Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln
50          55          60

```

```

Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
65          70          75          80

```

```

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
85          90          95

```

```

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
100          105

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```

<210> 52
<211> 38
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic

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<400> 52
tctagaattc acgcgtccac catggactgg acctggag      38

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<210> 53
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 53
 tctagaattc acgcgtccac catggacaca ctttgctaca c 41

<210> 54
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 54
 tctagaattc acgcgtccac catggagttt gggctgagct gg 42

<210> 55
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 55
 tctagaattc acgcgtccac catgaaacac ctgtggttct tcct 44

<210> 56
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 56
 tctagaattc acgcgtccac catgggggtca accgccatcc t 41

<210> 57
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 57
 tctagaattc acgcgtccac catgtctgtc tccttcctca tctt 44

<210> 58
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 58
 gcctgagttc cacgacaccg tcac 24

 <210> 59
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 59
 ggggaaaagg gttggggcgg atgc 24

 <210> 60
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 60
 gaggggccct tggtcgacgc tgaggagacg gtgaccagg 39

 <210> 61
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 61
 gaggggccct tggtcgacgc tgaagagacg gtgaccattg 40

 <210> 62
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 62
 gaggggccct tggtcgacgc tgaggagacg gtgaccgtg 39

<210> 63
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 63
 tctagaattc acgcgtccac catggacatg aggggtccccg ctcag 45

 <210> 64
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 64
 tctagaattc acgcgtccac catgaggctc cctgctcagc 40

 <210> 65
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 65
 tctagaattc acgcgtccac catggaagcc ccagcgcagc tt 42

 <210> 66
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 66
 tctagaattc acgcgtccac catggtgttg cagaccagc t 41

 <210> 67
 <211> 41
 <212> DNA
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<210> 78
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<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
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<222> (34)..(37)
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<220>
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<400> 78
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<400> 79
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<210> 80
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<400> 80
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